1812

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/599,974B*

DATE: 06/19/97
TIME: 15:16:20

INPUT SET: S18492.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i) APPLICANT: Friedman, Jeffrey M.
 6                       Lee, Gwo-Hua
 7                       Proenca, Ricardo
 8
 9       (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
10               ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
11
12      (iii) NUMBER OF SEQUENCES: 54
13
14       (iv) CORRESPONDENCE ADDRESS:
15            (A) ADDRESSEE: David A. Jackson, Esq.
16            (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
17                    Floor
18            (C) CITY: Hackensack
19            (D) STATE: New Jersey
20            (E) COUNTRY: USA
21            (F) ZIP: 07601
22
23        (v) COMPUTER READABLE FORM:
24            (A) MEDIUM TYPE: Floppy disk
25            (B) COMPUTER: IBM PC compatible
26            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29       (vi) CURRENT APPLICATION DATA:
30            (A) APPLICATION NUMBER: US 08/599,974
31            (B) FILING DATE: 14-FEB-1996
32            (C) CLASSIFICATION:
33
34      (vii) PRIOR APPLICATION DATA:
35            (A) APPLICATION NUMBER: US 08/586,594
36            (B) FILING DATE: 16-JAN-1996
37            (C) CLASSIFICATION:
38
39     (viii) ATTORNEY/AGENT INFORMATION:
40            (A) NAME: Jackson Esq., David A.
41            (B) REGISTRATION NUMBER: 26,742
42            (C) REFERENCE/DOCKET NUMBER: 600-1-162 CP1
43
44       (ix) TELECOMMUNICATION INFORMATION:
45            (A) TELEPHONE: 201-487-5800
46            (B) TELEFAX: 201-343-1684
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INPUT SET: S18492.raw

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47
48
49    (2) INFORMATION FOR SEQ ID NO:1:
50
51          (i) SEQUENCE CHARACTERISTICS:
52                (A) LENGTH: 2529 base pairs
53                (B) TYPE: nucleic acid
54                (C) STRANDEDNESS: double
55                (D) TOPOLOGY: linear
56
57        (ii) MOLECULE TYPE: cDNA
58
59       (iii) HYPOTHETICAL: NO
60
61        (iv) ANTI-SENSE: NO
62
63
64       (vii) IMMEDIATE SOURCE:
65                (B) CLONE: A15 (OB-Ra)
66
67
68
69        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70
71    GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA GGCGCTCTCG          60
72
73    CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG TTGCTTTGGG         120
74
75    AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA GACACTGGCT         180
76
77    TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG         240
78
79    ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA GAACCCCTTC         300
80
81    AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT AGATGATTCG         360
82
83    CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGGA         420
84
85    TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT GATGTATTTG         480
86
87    GAAATCACAT CTGCCGGTGT GAGTTTTCAG TCACCTCTGA TGTCACTGCA GCCCATGCTT         540
88
89    GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA TGGTAATTTA         600
90
91    AAGATTTCTT GGGACAGCCA AACAATGGCA CCATTTCCGC TTCAATATCA GGTGAAATAT         660
92
93    TTAGAGAATT CTACAATTGT AAGAGAGGCT GCTGAAATTG TCTCAGCTAC ATCTCTGCTG         720
94
95    GTAGACAGTG TGCTTCCTGG ATCTTCATAT GAGGTCCAGG TGAGGAGCAA GAGACTGGAT         780
96
97    GGTTCAGGAG TCTGGAGTGA CTGGAGTTCA CCTCAAGTCT TTACCACACA AGATGTTGTG         840
98
99    TATTTTCCAC CCAAAATTCT GACTAGTGTT GGATCGAATG CTTCTTTTCA TTGCATCTAC         900
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PATENT APPLICATION   *US/08/599,974B*

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101  AAAAACGAAA ACCAGATTAT CTCCTCAAAA CAGATAGTTT GGTGGAGGAA TCTAGCTGAG      960
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103  AAAATCCCTG AGATACAGTA CAGCATTGTG AGTGACCGAG TTAGCAAAGT TACCTTCTCC     1020
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105  AACCTGAAAG CCACCAGACC TCGAGGGAAG TTTACCTATG ACGCAGTGTA CTGCTGCAAT     1080
106
107  GAGCAGGCGT GCCATCACCG CTATGCTGAA TTATACGTGA TCGATGTCAA TATCAATATA     1140
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109  TCATGTGAAA CTGACGGGTA CTTAACTAAA ATGACTTGCA GATGGTCACC CAGCACAATC     1200
110
111  CAATCACTAG TGGGAAGCAC TGTGCAGCTG AGGTATCACA GGCGCAGCCT GTATTGTCCT     1260
112
113  GATAGTCCAT CTATTCATCC TACGTCTGAG CCCAAAAACT GCGTCTTACA GAGAGACGGC     1320
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115  TTTTATGAAT GTGTTTTCCA GCCAATCTTT CTATTATCTG GCTATACAAT GTGGATCAGG     1380
116
117  ATCAACCATT CTTTAGGTTC ACTTGACTCG CCACCAACGT GTGTCCTTCC TGACTCCGTA     1440
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119  GTAAACCAC TACCTCCATC TAACGTAAAA GCAGAGATTA CTGTAAACAC TGGATTATTG     1500
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121  AAAGTATCTT GGGAAAAGCC AGTCTTTCCG GAGAATAACC TTCAATTCCA GATTCGATAT     1560
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123  GGCTTAAGTG GAAAAGAAAT ACAATGGAAG ACACATGAGG TATTCGATGC AAAGTCAAAG     1620
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125  TCTGCCAGCC TGCTGGTGTC AGACCTCTGT GCAGTCTATG TGGTCCAGGT TCGCTGCCGG     1680
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127  CGGTTGGATG GACTAGGATA TTGGAGTAAT TGGAGCAGTC CAGCCTATAC GCTTGTCATG     1740
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129  GATGTAAAAG TTCCTATGAG AGGGCCTGAA TTTTGGAGAA AAATGGATGG GGACGTTACT     1800
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131  AAAAAGGAGA GAAATGTCAC CTTGCTTTGG AAGCCCCTGA CGAAAAATGA CTCACTGTGT     1860
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133  AGTGTGAGGA GGTACGTGGT GAAGCATCGT ACTGCCCACA ATGGGACGTG GTCAGAAGAT     1920
134
135  GTGGGAAATC GGACCAATCT CACTTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT     1980
136
137  CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC     2040
138
139  ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC     2100
140
141  ATCCTTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG     2160
142
143  AAGATCCTTA ATGAAGATGA TGGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG     2220
144
145  TTTTATATCC ACGATAATTT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA     2280
146
147  TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC     2340
148
149  AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTC CTCTTGTGTC     2400
150
151  CTACTGCTCG GAACACTGTT AATTTCACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT     2460
152
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153   GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC   2520
154
155   ACTCTTTGA                                                          2529
156
157   (2) INFORMATION FOR SEQ ID NO:2:
158
159        (i) SEQUENCE CHARACTERISTICS:
160             (A) LENGTH: 842 amino acids
161             (B) TYPE: amino acid
162             (C) STRANDEDNESS: Not Relevant
163             (D) TOPOLOGY: Not Relevant
164
165     (ii) MOLECULE TYPE: protein
166
167    (iii) HYPOTHETICAL: NO
168
169     (iv) ANTI-SENSE: NO
170
171
172    (vii) IMMEDIATE SOURCE:
173             (B) CLONE: OB-Ra
174
175
176
177     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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179        Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
180        1               5               10              15
181
182        Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
183                20              25              30
184
185        Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
186                35              40              45
187
188        Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
189             50              55              60
190
191        Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
192        65              70              75              80
193
194        Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
195                     85              90              95
196
197        Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
198                100             105             110
199
200        Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Leu Lys Asp Ser
201             115             120             125
202
203        Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
204             130             135             140
205
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PATENT APPLICATION *US/08/599,974B*

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206       Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu
207       145             150             155                     160
208
209       Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
210                   165             170                 175
211
212       Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
213                   180             185                 190
214
215       Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
216               195             200                 205
217
218       Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
219           210             215                 220
220
221       Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
222       225             230                 235                     240
223
224       Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
225                   245             250                 255
226
227       Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
228                   260             265                 270
229
230       Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
231               275             280                 285
232
233       Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
234           290             295                 300
235
236       Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
237       305             310                 315                     320
238
239       Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
240                   325             330                 335
241
242       Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
243               340             345                 350
244
245       Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
246               355             360                 365
247
248       Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
249           370             375                 380
250
251       Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
252       385             390                 395                     400
253
254       Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
255                   405             410                 415
256
257       Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
258                   420             425                 430
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/599,974B*

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